



1646

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/976,472

DATE: 02/25/2002

TIME: 13:58:39

Input Set : A:\2932-B seq.txt

Output Set: N:\CRF3\02252002\I976472.raw

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3 <110> APPLICANT: SIMS, John E.
4   RENSHAW, Blair R.
6 <120> TITLE OF INVENTION: IL-1 ETA DNA AND POLYPEPTIDES
8 <130> FILE REFERENCE: 2932-B
10 <140> CURRENT APPLICATION NUMBER: 09/976,472
11 <141> CURRENT FILING DATE: 2001-10-11
13 <150> PRIOR APPLICATION NUMBER: PCT/US00/14435
14 <151> PRIOR FILING DATE: 2000-05-25
16 <150> PRIOR APPLICATION NUMBER: 60/162,331
17 <151> PRIOR FILING DATE: 1999-10-29
19 <150> PRIOR APPLICATION NUMBER: 60/135,758
20 <151> PRIOR FILING DATE: 1999-05-25
22 <160> NUMBER OF SEQ ID NOS: 2
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 585
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (112)..(585)
34 <223> OTHER INFORMATION:
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40 caccaccatc tgatctatct tgttctcttc acaaaaggct ctgaagacat c atg aac      117
41                                     Met Asn
42                                     1
44 cca caa cgg gag gca gca ccc aaa tcc tat gct att cgt gat tct cga      165
45 Pro Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp Ser Arg
46      5              10              15
48 cag atg gtg tgg gtc ctg agt gga aat tct tta ata gca gct cct ctt      213
49 Gln Met Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala Pro Leu
50      20              25              30
52 agc cgc agc att aag cct gtc act ctt cat tta ata gcc tgt aga gac      261
53 Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys Arg Asp
54 35              40              45              50
56 aca gaa ttc agt gac aag gaa aag ggt aat atg gtt tac ctg gga atc      309
57 Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu Gly Ile
58      55              60              65
60 aag gga aaa gat ctc tgt ctc ttc tgt gca gaa att cag ggc aag cct      357
61 Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly Lys Pro
62      70              75              80
64 act ttg cag ctt aag gaa aaa aat atc atg gac ctg tat gtg gag aag      405

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65 Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val Glu Lys
66      85                      90                      95
68 aaa gca cag aag ccc ttt ctc ttt ttc cac aat aaa gaa ggc tcc act      453
69 Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly Ser Thr
70      100                      105                      110
72 tct gtc ttt cag tca gtc tct tac cct ggc tgg ttc ata gcc acc tcc      501
73 Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala Thr Ser
74 115                      120                      125                      130
76 acc aca tca gga cag ccc atc ttt ctc acc aag gag aga ggc ata act      549
77 Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly Ile Thr
78      135                      140                      145
80 aat aac act aac ttc tac tta gat tct gtg gaa taa      585
81 Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
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85 <210> SEQ ID NO: 2
86 <211> LENGTH: 157
87 <212> TYPE: PRT
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97      20                      25                      30
100 Pro Leu Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys
101      35                      40                      45
104 Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu
105      50                      55                      60
108 Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly
109 65                      70                      75                      80
112 Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val
113      85                      90                      95
116 Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly
117      100                      105                      110
120 Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
121      115                      120                      125
124 Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
125      130                      135                      140
128 Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
129 145                      150                      155

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VERIFICATION SUMMARY

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